S. Jant

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/506,079 B_

Source: _1642_

Date Processed by STIC: _4-17-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

1642

```
         RAW SEQUENCE LISTING              DATE: 04/17/2001
         PATENT APPLICATION:  US/09/506,079B     TIME: 14:34:16

         Input Set : A:\SEQUENCE 3-28-01.txt
         Output Set: N:\CRF3\04172001\I506079B.raw

         SEQUENCE LISTING
  2 (1) GENERAL INFORMATION:
C--> 4      (i) APPLICANT: Clinton, Gail M., Adam Evans and William D. Henner
  6     (ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
  8    (iii) NUMBER OF SEQUENCES: 10
 10     (iv) CORRESPONDENCE ADDRESS:
 11          (A) ADDRESSEE: DAVIS WRIGHT TREMAINE
 12          (B) STREET: 1501 Fourth Avenue, 2600 Century Square
 13          (C) CITY: Seattle
 14          (D) STATE: Washington
 15          (E) COUNTRY: U.S.A.
 16          (F) ZIP: 98101
 18      (v) COMPUTER READABLE FORM:
 19          (A) MEDIUM TYPE: Floppy disk
 20          (B) COMPUTER: PC compatible
 21          (C) OPERATING SYSTEM: Windows95
 22          (D) SOFTWARE: Word
 24     (vi) CURRENT APPLICATION DATA:
C--> 25          (A) APPLICATION NUMBER: US/09/506,079B
C--> 26          (B) FILING DATE: 16-Feb-2000
 27          (C) CLASSIFICATION:
 29    (viii) ATTORNEY/AGENT INFORMATION:
 30          (A) NAME: Davison, Barry L.
 31          (B) REGISTRATION NUMBER: 47,309
 32          (C) REFERENCE/DOCKET NUMBER: 49321-16
 34     (ix) TELECOMMUNICATION INFORMATION:
 35          (A) TELEPHONE: 206 628 7621
 36          (B) TELEFAX: 206 628 7699
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
 59 (2) INFORMATION FOR SEQ ID NO: 2:
 61      (i) SEQUENCE CHARACTERISTICS:
 62          (A) LENGTH: 419
 63          (B) TYPE: amino acid
 64          (C) STRANDEDNESS: single
 65          (D) TOPOLOGY: unknown
 66     (ii) MOLECULE TYPE: polypeptide
 67     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 69 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 70                 5                  10                  15
 71 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys
 72                20                  25                  30
 73 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
 74                35                  40                  45
 75 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
```

Input Set : A:\SEQUENCE 3-28-01.txt
Output Set: N:\CRF3\04172001\I506079B.raw

```
    76      50                    55                    60
    77 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
    78 65                    70                    75                    80
    79 Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu
    80                    85                    90                    95
    81 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
    82                   100                   105                   110
E--> 83 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Agn Agn Thr Thr Pro
    84            115                   120                   125
    85 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
    86       130                   135                   140
    87 Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
    88 145                   150                   155                   160
    89 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
    90                   165                   170                   175
    91 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
    92                   180                   185                   190
    93 His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
    94            195                   200                   205
    95 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    96       210                   215                   220
    97 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
    98 225                   230                   235                   240
    99 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
   100                   245                   250                   255
   101 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
   102            260                   265                   270
   103 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg
   104       275                   280                   285
   105 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu
   106       290                   295                   300
   107 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
   108 305                   310                   315                   320
   109 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
   110            325                   330                   335
W--> 111 Pro Cys Ala Arg Gly His Ser Xaa Xaa Pro Arg Pro Ala Ala Val
   112            340                   345                   350
W--> 113 Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser
   114       355                   360                   365
W--> 115 Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro
   116       370                   375                   380
W--> 117 Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
   118 385                   390                   395                   400
W--> 119 Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg
   120            405                   410                   415
   121 Tyr Glu Gly
```

Invalid amino acid designators (handwritten annotation pointing to "Agn Agn" at position 123-124)

VERIFICATION SUMMARY   DATE: 04/17/2001
PATENT APPLICATION: US/09/506,079B   TIME: 14:34:17

Input Set : A:\SEQUENCE 3-28-01.txt
Output Set: N:\CRF3\04172001\I506079B.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:45 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:83 M:330 E: (2) Invalid Amino Acid Designator, 2
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:130 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:142 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:153 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:165 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:176 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:187 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:198 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:210 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10